

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Boodhoo, Amechand
Seehra, Jasbir
Shaw, Gray
Sako, Dianne

(ii) TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND
RELATED PROTEASES, AND THERAPEUTIC USES
THEREOF

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.
(B) REGISTRATION NUMBER: 32,724
(C) REFERENCE/DOCKET NUMBER: GI5293A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8224
(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Thr	Asn	Thr	Pro	Glu	Gln	Asp	Arg	Tyr	Leu	Gln	Ala	Lys	Lys	Tyr	Ile
1				5					10					15	
Glu	Phe	Tyr	Val	Val	Val	Asp	Asn	Val	Met	Tyr	Arg	Lys	Tyr		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr	Asn	Thr	Pro	Glu	Gln	Asp	Arg	Tyr	Leu	Gln	Ala	Lys	Lys	Tyr	Ile
1				5					10					15	
Glu	Phe	Tyr	Val	Val	Val	Asp	Asn	Val	Met	Tyr	Arg	Lys	Tyr	Thr	Gly
			20					25					30		
Lys	Leu	His	Val	Ile	Thr	Xaa	Xaa	Val	Tyr	Glu	Met	Asn	Ala	Leu	Asn
			35					40					45		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu	Ala	Thr	Glu	Tyr	Glu	Tyr	Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln	Ala	Thr	Glu	Tyr	Glu	Tyr	Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 78..1940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGTCAATAGG AGAAGAGCTC AGGTTGGCTT GGAAGCAGAA AGAGATTCCT GTCCACCACT 60
CCAATCCAGG CTCCAAAATG ATCCAAGCTC TCTTGGTAGC TATATGCTTA GCGGTTTTTC 120
CATATCAAGG GAGCTCTATA ATCCTGGAAT CCGGGAATGT TAATGATTAT GAAGTAGTGT 180
ATCCACAAAA AGTGCCTGCA TTGTCCAAAG GAGGAGTTCA GAATCCTCAG CCAGAGACCA 240
AGTATGAAGA TACAATGCAA TATGAATTTC ACGTGAACGG AGAGCCAGTG GTCCTTCACT 300
TAGAAAGAAA TAAAGGACTT TTTTCAGAAG ATTACACTGA AACTCATTAT GCCCCTGATG 360
GCAGAGAAAT TACAACAAGC TCTCCAGTTC AGGATCACTG CTATTATCAT GGTACATTC 420
AGAATGAAGC TGACTCAAGT GCAGTCATCA GTGCATGTGA TGGCTTGAAA GGACATTTCA 480
AGCATCAAGG GGAGACATAC TTTATTGAGC CCTTGGAGCT TTCTGACAGT GAAGCCCATG 540
CAATATACAA AGATGAAAAT GTAGAAGAAG AGGAAGAGAT CCCCAAATC TGTGGGGTTA 600
CCCAGACTAC TTGGGAATCA GATGAGCCGA TTGAAAAGTC CTCTCAGTTA ACTAATACTC 660
CTGAACAAGA CAGGTACTTG CAGGCCAAAA AATACATCGA GTTTTACGTG GTTGTGGACA 720
ATGTAATGTA CMGRAAATAC ACCGGCAAGT TACATGTTAT AACAAGAAGA GTATATGAAA 780
TGGTCAACGC TTAAATACG ATGTACAGAC GTTTGAATTT TCACATAGCA CTGATTGGCC 840
TAGAAATTG GTCCAACGGA AATGAGATTA ATGTGCAATC AGACGTGCAG GCCACTTTGG 900
ACTTATTTGG AGAATGGAGA GAAAATAAAT TGCTGCCACG CAAAAGGAAT GATAATGCTC 960
AGTTACTCAC GAGCACTGAG TTCAATGGAA CTAACACAGG ACTTGGTTAC ATAGGCTCCC 1020
TCTGTAGTCC GAAGAAATCT GTGGCAGTTG TTCAGGATCA TAGCAAAAGC ACAAGCATGG 1080
TGGCAATTAC AATGGCCCAT CAGATGGGTC ATAATCTGGG CATGAATGAT GACAGAGCTT 1140
CCTGTACTTG TGTTCTAAC AAATGCATTA TGTCTACAAA ATATTATGAA TCTCTTTCTG 1200

AGTTCAGCTC TTGTAGTGTC CAGGAACATC GGGAGTATCT TCTTAGAGAC AGACCACAAT 1260
 GCATTCTCAA CAAACCCTCG CGCAAAGCTA TTGTTACACC TCCAGTTTGT GGAAATTACT 1320
 TTGTGGAGCG GGGAGAAGAA TGTGACTGTG GCTCTCCTGA GGATTGTCAA AATACCTGCT 1380
 GTGATGCTGC AACTTGTAAG CTGCAACATG AGGCACAGTG TGACTCTGGA GAGTGTGTG 1440
 AGAAATGCAA ATTTAAGGGA GCAGGAGCAG AATGCCGGGC AGCAAAGAAT GACTGTGACT 1500
 TTCCTGAACT CTGCACTGGC CGATCTGCTA AGTGTCCCAA GGACAGCTTC CAGAGGAATG 1560
 GACATCCATG CCAAAACAAC CAAGGTTACT GCTACAATGG GACATGTCCC ACCTTGACAA 1620
 ACCAATGTGC TACTCTCTGG GGGCCAGGTG CAAAAATGTC TCCAGGTTTA TGTTTTATGT 1680
 TGAAGTGGAA TGCCCGAAGT TGTGGCTTGT GCAGAAAGGA AAATGGCAGA AAGATTCTAT 1740
 GTGCAGCAAA GGATGTAAAG TGTGGCAGGT TATTTTGCAA AAAGAAAAAC TCGATGATAT 1800
 GCCACTGCCC ACTCCATCAA AGGACCCAAA TTATGGAATG GTTGACCTG GAACAAAATG 1860
 TGGAGTTAAA AAGGTGTGCA GAAACAGGCA ATGTGTTAAA GTATAGACAG CCAACTGATC 1920
 AAGCACTGCT TCTCTCAATT TGATTTTGGG GATCCTCCTT CCAGAAGGCT TTCCTCAAGT 1980
 CCAAAGAGAC CCATCTGTCT TTATCCTACT AGTAAATCAC TCTTAGCTTT CAAAAAAAAA 2040
 AAAAGTCGAC 2050

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ile Gln Ala Leu Leu Val Ala Ile Cys Leu Ala Val Phe Pro Tyr

1	5	10	15
Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu			
20	25	30	
Val Val Tyr Pro Gln Lys Val Pro Ala Leu Ser Lys Gly Gly Val Gln			
35	40	45	
Asn Pro Gln Pro Glu Thr Lys Tyr Glu Asp Thr Met Gln Tyr Glu Phe			
50	55	60	
His Val Asn Gly Glu Pro Val Val Leu His Leu Glu Arg Asn Lys Gly			
65	70	75	80
Leu Phe Ser Glu Asp Tyr Thr Glu Thr His Tyr Ala Pro Asp Gly Arg			
85	90	95	
Glu Ile Thr Thr Ser Ser Pro Val Gln Asp His Cys Tyr Tyr His Gly			
100	105	110	
Tyr Ile Gln Asn Glu Ala Asp Ser Ser Ala Val Ile Ser Ala Cys Asp			
115	120	125	
Gly Leu Lys Gly His Phe Lys His Gln Gly Glu Thr Tyr Phe Ile Glu			
130	135	140	
Pro Leu Glu Leu Ser Asp Ser Glu Ala His Ala Ile Tyr Lys Asp Glu			
145	150	155	160
Asn Val Glu Glu Glu Glu Glu Ile Pro Lys Ile Cys Gly Val Thr Gln			
165	170	175	
Thr Thr Trp Glu Ser Asp Glu Pro Ile Glu Lys Ser Ser Gln Leu Thr			
180	185	190	
Asn Thr Pro Glu Gln Asp Arg Tyr Leu Gln Ala Lys Lys Tyr Ile Glu			
195	200	205	
Phe Tyr Val Val Val Asp Asn Val Met Tyr Arg Lys Tyr Thr Gly Lys			
210	215	220	
Leu His Val Ile Thr Arg Arg Val Tyr Glu Met Val Asn Ala Leu Asn			
225	230	235	240
Thr Met Tyr Arg Arg Leu Asn Phe His Ile Ala Leu Ile Gly Leu Glu			
245	250	255	

Ile Trp Ser Asn Gly Asn Glu Ile Asn Val Gln Ser Asp Val Gln Ala
 260 265 270
 Thr Leu Asp Leu Phe Gly Glu Trp Arg Glu Asn Lys Leu Leu Pro Arg
 275 280 285
 Lys Arg Asn Asp Asn Ala Gln Leu Leu Thr Ser Thr Glu Phe Asn Gly
 290 295 300
 Thr Thr Thr Gly Leu Gly Tyr Ile Gly Ser Leu Cys Ser Pro Lys Lys
 305 310 315 320
 Ser Val Ala Val Val Gln Asp His Ser Lys Ser Thr Ser Met Val Ala
 325 330 335
 Ile Thr Met Ala His Gln Met Gly His Asn Leu Gly Met Asn Asp Asp
 340 345 350
 Arg Ala Ser Cys Thr Cys Gly Ser Asn Lys Cys Ile Met Ser Thr Lys
 355 360 365
 Tyr Tyr Glu Ser Leu Ser Glu Phe Ser Ser Cys Ser Val Gln Glu His
 370 375 380
 Arg Glu Tyr Leu Leu Arg Asp Arg Pro Gln Cys Ile Leu Asn Lys Pro
 385 390 395 400
 Ser Arg Lys Ala Ile Val Thr Pro Pro Val Cys Gly Asn Tyr Phe Val
 405 410 415
 Glu Arg Gly Glu Glu Cys Asp Cys Gly Ser Pro Glu Asp Cys Gln Asn
 420 425 430
 Thr Cys Cys Asp Ala Ala Thr Cys Lys Leu Gln His Glu Ala Gln Cys
 435 440 445
 Asp Ser Gly Glu Cys Cys Glu Lys Cys Lys Phe Lys Gly Ala Gly Ala
 450 455 460
 Glu Cys Arg Ala Ala Lys Asn Asp Cys Asp Phe Pro Glu Leu Cys Thr
 465 470 475 480
 Gly Arg Ser Ala Lys Cys Pro Lys Asp Ser Phe Gln Arg Asn Gly His
 485 490 495
 Pro Cys Gln Asn Asn Gln Gly Tyr Cys Tyr Asn Gly Thr Cys Pro Thr

500	505	510
Leu Thr Asn Gln Cys Ala Thr Leu Trp Gly Pro Gly Ala Lys Met Ser		
515	520	525
Pro Gly Leu Cys Phe Met Leu Asn Trp Asn Ala Arg Ser Cys Gly Leu		
530	535	540
Cys Arg Lys Glu Asn Gly Arg Lys Ile Leu Cys Ala Ala Lys Asp Val		
545	550	555 560
Lys Cys Gly Arg Leu Phe Cys Lys Lys Lys Asn Ser Met Ile Cys His		
565	570	575
Cys Pro Leu His Gln Arg Thr Gln Ile Met Glu Trp Leu His Leu Glu		
580	585	590
Gln Asn Val Glu Leu Lys Arg Cys Ala Glu Thr Gly Asn Val Leu Lys		
595	600	605
Tyr Arg Gln Pro Thr Asp Gln Ala Leu Leu Leu Ser Ile		
610	615	620

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACCA GT CAACAGGAGA AAAGCTCAGG TTGGCTTGGA AGCAGAAAGA GATTCCTGTC	60
CACCAGTCCA ATCCAGGCTC CAAAATGATC CAAGCTCTCT TGGTAATTAT ATGCTTAGCG	120
GTTTTTCCAT ATCAAGGGAG CTCTATAATC CTGGAATCTG GGAATGTTAA TGATTATGAA	180
GTTGTGTATC CACAAAAAGT GCCTGCATTG CTCAAAGGAG GAGTTCAGAA TCCTCAGCCA	240

GAGACCAAGT ATGAAGATAC AATGCAATAT GAATTTCAAG TGAATGGAGA GCCAGTAGTC	300
CTTCACTTAG AAAGAAATAA AGGACTTTTT TCAGAAGATT ACGTGAAAC TCATTATGCC	360
CCTGATGGCA GAGAAATTAC AACAAGCCCT CCGGTTGAGG ATCACTGCTA TTATCATGGT	420
TACATTGAGA ATGAAGCTGA CTCAAGTGCA ATCATCAGTG CATGTGATGG CTTGAAAGGA	480
CATTTCAAGC ATCAAGGGGA GACATACTTT ATTGAGCCCT TGAAGCTTTT CGACACTGAA	540
TCTCATGCAA TCTACAAAGA TGAAAATGTA GAAAACGAGG ATGAGACCCC CGAAACCTGT	600
GGGGTAACCG AGACTACTTG GGAGTCAGAT GAGTCCATCG AAAAGACCTC TCAGTTAACT	660
AACACTCCTG AACAAGACGG GACTTGCAG GCCAAAAAAT ACATCGAGTT TTACGTGGTT	720
GTGGACAACA GAATGTACAG GTATTACAAA CGCAATGAAC CTGCTATAAA AAGAAGAGTA	780
TATGAAATGG TCAACGCTGT AAATACGAAG TACAGACCTT TGAAAATTCA CATAACACTG	840
ATTGGCCTAG AAATTTGGTC CAACCATGAT AAGTTTGAAG TGAAGCCAGT AGCGGGTGCC	900
ACTTTGAAAT CATTTGAGA TTGGAGAGAA ACAGTTTGC TGCCACGCAA AAGGAATGAT	960
AACGCTCAGT TACTCACGGG CATTGACTTC AATGGAACG TTGTGGGAAT TGCTTACAG	1020
GGCACCTCT GCACTCAGAA TTCTGTAGCA GTTGTTCAGG ATTATAACCG AAAAATAAGC	1080
ATGGTGGCAT CTACAATGGC CCATGAGTTG GGTGATAATC TGGGCCTCA TCATGACGGA	1140
GCTTCCTGTA TTTGCAGTCT TAGACCATGC ATTATGTCTA AGGGACGGAC TGCACCTGCC	1200
TTTCAGTTCA GCTCTGTAG TGTCCGGGAG TATCGGGAGT ATCTTCTTAG AGAAAGACCA	1260
CAATGCATTC TCAACAAACC CTTGAGCACA GATACTGTTT CACCTGCAAT TTGTGGAAAT	1320
TACTTTGTGG AGGAGGGAGA AGAATGTGAC TGTGGCTCTC CTGCGGATTG TCAAAGTGCC	1380
TGCTGCGATG CTGCAACTTG TTAGTTTAAG GGAGAAGAAG CAGAATGCCG GGCAGCAAAG	1440
GATGACTGTG ACTTGCTGA ACTCTGCACT GGCCGATCTG TGGAGTGCC CACGGACAGC	1500
TTGCAGAAGA ATGGACATCC ATGTCAAAC AACAAAGGT ACTGCTACAA TGGGGCATGT	1560
CCCACCTTCA CAAACCAATG TATTGCTCTC ATGGGGACAG ATTTTACTGT GAGTCCAGAT	1620

GGATGTTTTG ACTTGAACGT GAGAGGGAAT GATGTAAGCC ACTGCAGAAA GGAAAATGGT 1680
GCAAAGATTG CATGTGCAGC AAAGGATGTA AAGTGTGGCA GGTATACTG CACAGAGAGA 1740
GACACAATGT CATGCCGATT CCCACTGGAC CCAGATGGTG TAATGGCTGA ACCTGGAACA 1800
AAATGTGGAG ATGGAATGGT GTGCAGCAAC GGTCAGTGTG TTAATGTGCA GACAGCCTAC 1860
TGATCAAGCA CTGGCTTCTC TCAATTTGAT TTTGGAGATC CTCCTTCCAG AACGCTTCCC 1920
TCAAGTCCAA AGAGACCCAT CTGTCTTTAT CCTACTAGTA AATCACTCTT AGCTTTCAGA 1980
TGGTATCTAA AATTTATAAT ATTTCTTCTC CATAATTTAA ACTGGTAATC TTTTGCTAAA 2040
ATCAGACCTT TTCCCTGCCA CAAAGCTCCA TGGTCATGTA CAGCACCAAA GGCTTATTTG 2100
CGAATAAGAA AAAAAAATGG CAATTTTACA GTTCCCAAT TGCAATGCAT ATTGAATGCA 2160
ACAAGCTCTG CCCTTTGAGC TGGCGTATTC AAAGGCAATG CTCCTCTCC CAAAATTATA 2220
CGCTGGCTTT CCAAGATGTA GCTGCTTCCA TCAATAAACT ATTCTCATTC TGCAAAAAAA 2280
AAAAAAAAAA AGTCGAC 2297

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ile	Gln	Ala	Leu	Leu	Val	Ile	Ile	Cys	Leu	Ala	Val	Phe	Pro	Tyr
1					5				10				15		
Gln	Gly	Ser	Ser	Ile	Ile	Leu	Glu	Ser	Gly	Asn	Val	Asn	Asp	Tyr	Glu
				20				25					30		
Val	Val	Tyr	Pro	Gln	Lys	Val	Pro	Ala	Leu	Leu	Lys	Gly	Gly	Val	Gln

35	40	45
Asn Pro Gln Pro Glu Thr Lys Tyr Glu Asp Thr Met Gln Tyr Glu Phe		
50	55	60
Gln Val Asn Gly Glu Pro Val Val Leu His Leu Glu Arg Asn Lys Gly		
65	70	75 80
Leu Phe Ser Glu Asp Tyr Thr Glu Thr His Tyr Ala Pro Asp Gly Arg		
85	90	95
Glu Ile Thr Thr Ser Pro Pro Val Gln Asp His Cys Tyr Tyr His Gly		
100	105	110
Tyr Ile Gln Asn Glu Ala Asp Ser Ser Ala Ile Ile Ser Ala Cys Asp		
115	120	125
Gly Leu Lys Gly His Phe Lys His Gln Gly Glu Thr Tyr Phe Ile Glu		
130	135	140
Pro Leu Lys Leu Phe Asp Ser Glu Ser His Ala Ile Tyr Lys Asp Glu		
145	150	155 160
Asn Val Glu Asn Glu Asp Glu Thr Pro Glu Thr Cys Gly Val Thr Glu		
165	170	175
Thr Thr Trp Glu Ser Asp Glu Ser Ile Glu Lys Thr Ser Gln Leu Thr		
180	185	190
Asn Thr Pro Glu Gln Asp Gly Tyr Leu Gln Ala Lys Lys Tyr Ile Glu		
195	200	205
Phe Tyr Val Val Val Asp Asn Arg Met Tyr Arg Tyr Tyr Lys Arg Asn		
210	215	220
Glu Pro Ala Ile Lys Arg Arg Val Tyr Glu Met Val Asn Ala Val Asn		
225	230	235 240
Thr Lys Tyr Arg Pro Leu Lys Ile His Ile Thr Leu Ile Gly Leu Glu		
245	250	255
Ile Trp Ser Asn His Asp Lys Phe Glu Val Lys Pro Val Ala Gly Ala		
260	265	270
Thr Leu Lys Ser Phe Arg Asp Trp Arg Glu Thr Val Leu Leu Pro Arg		
275	280	285

Lys Arg Asn Asp Asn Ala Gln Leu Leu Thr Gly Ile Asp Phe Asn Gly
 290 295 300
 Thr Val Val Gly Ile Ala Tyr Thr Gly Thr Leu Cys Thr Gln Asn Ser
 305 310 315 320
 Val Ala Val Val Gln Asp Tyr Asn Arg Lys Ile Ser Met Val Ala Ser
 325 330 335
 Thr Met Ala His Glu Leu Gly His Asn Leu Gly Leu His His Asp Gly
 340 345 350
 Ala Ser Cys Ile Cys Ser Leu Arg Pro Cys Ile Met Ser Lys Gly Arg
 355 360 365
 Thr Ala Pro Ala Phe Gln Phe Ser Ser Cys Ser Val Arg Glu Tyr Arg
 370 375 380
 Glu Tyr Leu Leu Arg Glu Arg Pro Gln Cys Ile Leu Asn Lys Pro Leu
 385 390 395 400
 Ser Thr Asp Thr Val Ser Pro Ala Ile Cys Gly Asn Tyr Phe Val Glu
 405 410 415
 Glu Gly Glu Glu Cys Asp Cys Gly Ser Pro Ala Asp Cys Gln Ser Ala
 420 425 430
 Cys Cys Asp Ala Ala Thr Cys
 435

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGACCTCA GGTGGCTTG GAAGCAGAAA GAGATTCCTA TCCACCACTC CAATCCAGGC	60
TCCAAAATGA TCCAAGCTCT CTTGGTAGCT ATATGCTTAG CGGTTTTTCC ATATCAAGGG	120
AGCTCTATAA TCCTGGAATC CGGGAATGTT AATGATTATG AAGTAGTGTA TCCACAAAAA	180
GTGCCTGCAT TGTCCAAAGG AGGAGTTCAG AATCCTCAGC CAGAGACCAA GTATGAAGAT	240
ACAATGCAAT ATGAATTTC AGTGAATGGA GAGCCAGTAG TCCTTCACCT AGAAAGAAAT	300
AAAGGACTTT TTTCAGAAGA TTACTTGAA ACTCATTATG CCTCTGATGG CAGAGAAATT	360
ACAACAAGCC CACTCGTTCA GGATCACTGC TATTATCATG GTTACATTCA GAATGAAGCT	420
GACTIONAGTG CAGTCATCAG TGCATGCGAT GGCTTGAAAG GACATTTTGA GCTTCAAGGG	480
GAGACATACT TTATTGAACC CTTGAAGATT TCCGACAGTG AAGCCCATGC AATCTACAAA	540
GATGAAAATG TAGAAAACGA GGATGAGACC CCCGAAACCT GTGGGGTAAC CGAGACTACT	600
TGGGAGTCAG ATGAGTCCAT TGAAAAGACC TCTCAGTTAA CTAACACTCC TGAACAAGAC	660
AGTACTTGC AGGCCAAAAA ATACCTCGAG TTTTACGTGG TTGTGGACAA CATAATGTAC	720
AGGCATTACA AACGCGATAA ACCTGTTATA AAAAGAAGAG TATATGAAAT GATCAACACT	780
ATGAATATGG TGTACAATCG TTTGAATTTT CACATAGCAC TGATTGGCCT AGAAATTTGG	840
TCCAACAGAA ATGAGATTAA TGTGCAATCA GACGTGCAGG CCACTTTGGA CTTATTTGGA	900
GAATGGAGAG AAAAAAATT GCTGCCACGC AAAAGGAATG ATAATGCTCA GTTACTCACG	960
GGTATTGACT TCAAAGGAAC TCCTGTAGGA CTTGCTTACA TAGGTTCCAT CTGCAATCCG	1020
AAGAGTTCTG TAGCAGTTGT TCAGGATTAT AGCAGTAGAA CAAGCATGGT GGCAATTACA	1080
ATGGCCCATG AGATGGGTCA TAATATGGGC ATTCATCATG ACGGACCTTC CTGTACTTGT	1140
GGTTCTAACA AATGCGTTAT GTCTACAAGA CGTACTGAAC CTGCCTATCA GTTCAGCTCT	1200

TGTAGTGTCC GGGAACATCA GGAGTATCTT CTTAGAGACA GACCACAATG CATTCTCAAC	1260
AAACCCCTTGA GCACAGATAT TGTTTCACCT CCAATTTGTG GAAATAACTT TGTGGAGGTG	1320
GGAGAAGAAT GTGACTGTGG CTCTCCTGCG GATTGTCAAA GTGCCTGCTG CGACGCTACA	1380
ACTTGTA AAC TACAACCTCA TGCACAGTGT GACTCCGAAG GGTGTTGTGA GAAATGCAAA	1440
TTTAAGGGAG CAGGAGCAGA ATGCCGGGCA GCAAAGGATG ACTGTGACTT GCCTGAACTC	1500
TGCACTGGCC AATCTGCTGA GTGTCCCACA GACATCTTCC AGAGGAATGG ACTTCCATGC	1560
CAAAACAACG AAGGTTACTG CTACAATGGG AAATGCCCCA TCATGACAAA CCAATGTATT	1620
GCTCTCCGGG GACCAGGTGT AAAAGTATCT CGAGATAGCT GTTTTACATT GAACCAGAGA	1680
ACCAGTGGTT GTGGCTTGTG CAGAATGGAA TATGGTAGAA AGATTCCATG TGCAGCAAAG	1740
GATGTAAAGT GTGGCAGGTT ATTTTGCAAA AAGGGAAACT CGATGATATG CAACTGCTCA	1800
GTTTCACCAC GTGACCCAAG TTATGGAATG GTTGAACCTG GAACAAAATG TGGAGATGGA	1860
ATGGTGTGCA GCAACAGGCA GTGTGTTGAT GTGAAGACAG CCTACTGATC AAGCACTGGC	1920
TTCTCTCAAT TTGATTTTGG AGGTCTCCT TCCAGAACGC TTCCCTCAAG TCCAAAGAGA	1980
CCCATCTGTC TTTATCCTAC TAGTAAATCA CTCTTAGCTT TCAGATGGTA TCTAAAATTT	2040
AAAATATTTT TTCTCCATAA TTAAACTGG TAATCTTTTG CTAAAATCAG ACCTTTTCCC	2100
TGCCACAAAG CTCCATGGTC ATGTACAGCA CCAAAGGCTT ATTTGCTAAC AAGAAAAAAA	2160
ATGGCCATTT TACTGTTTGC CAATTGCAAT TCACATTTAA TGCAACAAGC TCTGCCCTTT	2220
GAGCTGGCGT ACTCAAAGGC AATGCTCCCT CTCCCAAAAT TATACGCTGG CTTTCCAAGA	2280
TGTAGCTGCT TCCATCAATA AACTATTCTC ATTCTGAAAA AAAAAAAAAAG TCGAC	2335

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ile	Gln	Ala	Leu	Leu	Val	Ala	Ile	Cys	Leu	Ala	Val	Phe	Pro	Tyr
1				5					10					15	
Gln	Gly	Ser	Ser	Ile	Ile	Leu	Glu	Ser	Gly	Asn	Val	Asn	Asp	Tyr	Glu
				20					25					30	
Val	Val	Tyr	Pro	Gln	Lys	Val	Pro	Ala	Leu	Ser	Lys	Gly	Gly	Val	Gln
				35					40					45	
Asn	Pro	Gln	Pro	Glu	Thr	Lys	Tyr	Glu	Asp	Thr	Met	Gln	Tyr	Glu	Phe
				50					55					60	
Gln	Val	Asn	Gly	Glu	Pro	Val	Val	Leu	His	Leu	Glu	Arg	Asn	Lys	Gly
				65					70					75	
Leu	Phe	Ser	Glu	Asp	Tyr	Thr	Glu	Thr	His	Tyr	Ala	Ser	Asp	Gly	Arg
									85					90	
Glu	Ile	Thr	Thr	Ser	Pro	Leu	Val	Gln	Asp	His	Cys	Tyr	Tyr	His	Gly
									100					105	
Tyr	Ile	Gln	Asn	Glu	Ala	Asp	Ser	Ser	Ala	Val	Ile	Ser	Ala	Cys	Asp
									115					120	
Gly	Leu	Lys	Gly	His	Phe	Glu	Leu	Gln	Gly	Glu	Thr	Tyr	Phe	Ile	Glu
									130					135	
														140	

Pro Leu Lys Ile Ser Asp Ser Glu Ala His Ala Ile Tyr Lys Asp Glu
 145 150 155 160

Asn Val Glu Asn Glu Asp Glu Thr Pro Glu Thr Cys Gly Val Thr Glu
 165 170 175

Thr Thr Trp Glu Ser Asp Glu Ser Ile Glu Lys Thr Ser Gln Leu Thr
 180 185 190

Asn Thr Pro Glu Gln Asp Arg Tyr Leu Gln Ala Lys Lys Tyr Leu Glu
 195 200 205

Phe Tyr Val Val Val Asp Asn Ile Met Tyr Arg His Tyr Lys Arg Asp
 210 215 220

Lys Pro Val Ile Lys Arg Arg Val Tyr Glu Met Ile Asn Thr Met Asn
 225 230 235 240

Met Val Tyr Asn Arg Leu Asn Phe His Ile Ala Leu Ile Gly Leu Glu
 245 250 255

Ile Trp Ser Asn Arg Asn Glu Ile Asn Val Gln Ser Asp Val Gln Ala
 260 265 270

Thr Leu Asp Leu Phe Gly Glu Trp Arg Glu Lys Lys Leu Leu Pro Arg
 275 280 285

Lys Arg Asn Asp Asn Ala Gln Leu Leu Thr Gly Ile Asp Phe Lys Gly
 290 295 300

Thr Pro Val Gly Leu Ala Tyr Ile Gly Ser Ile Cys Asn Pro Lys Ser
 305 310 315 320

Ser Val Ala Val Val Gln Asp Tyr Ser Ser Arg Thr Ser Met Val Ala
 325 330 335

Ile Thr Met Ala His Glu Met Gly His Asn Met Gly Ile His His Asp
 340 345 350

Gly Pro Ser Cys Thr Cys Gly Ser Asn Lys Cys Val Met Ser Thr Arg

355	360	365
Arg Thr Glu Pro Ala Tyr Gln Phe Ser Ser Cys Ser Val Arg Glu His		
370	375	380
Gln Glu Tyr Leu Leu Arg Asp Arg Pro Gln Cys Ile Leu Asn Lys Pro		
385	390	395 400
Leu Ser Thr Asp Ile Val Ser Pro Pro Ile Cys Gly Asn Asn Phe Val		
405	410	415
Glu Val Gly Glu Glu Cys Asp Cys Gly Ser Pro Ala Asp Cys Gln Ser		
420	425	430
Ala Cys Cys Asp Ala Thr Thr Cys Lys Leu Gln Pro His Ala Gln Cys		
435	440	445
Asp Ser Glu Gly Cys Cys Glu Lys Cys Lys Phe Lys Gly Ala Gly Ala		
450	455	460
Glu Cys Arg Ala Ala Lys Asp Asp Cys Asp Leu Pro Glu Leu Cys Thr		
465	470	475 480
Gly Gln Ser Ala Glu Cys Pro Thr Asp Ile Phe Gln Arg Asn Gly Leu		
485	490	495
Pro Cys Gln Asn Asn Glu Gly Tyr Cys Tyr Asn Gly Lys Cys Pro Ile		
500	505	510
Met Thr Asn Gln Cys Ile Ala Leu Arg Gly Pro Gly Val Lys Val Ser		
515	520	525
Arg Asp Ser Cys Phe Thr Leu Asn Gln Arg Thr Ser Gly Cys Gly Leu		
530	535	540
Cys Arg Met Glu Tyr Gly Arg Lys Ile Pro Cys Ala Ala Lys Asp Val		
545	550	555 560
Lys Cys Gly Arg Leu Phe Cys Lys Lys Gly Asn Ser Met Ile Cys Asn		
565	570	575

Cys Ser Val Ser Pro Arg Asp Pro Ser Tyr Gly Met Val Glu Pro Gly
580 585 590

Thr Lys Cys Gly Asp Gly Met Val Cys Ser Asn Arg Gln Cys Val Asp
595 600 605

Val Lys Thr Ala Tyr
610

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGTCAACAGG AGAAAAGCTC AGGTTGGCTT GGAAGCAGAA AGAGATTCCT GTCCACCAGT	60
CCAATCCAGG CTCCAAAATG ATCCAAGCTC TCTTGTAAT TATATGCTTA GTGGTTTTTC	120
CATATCAAGG GAGCTCTATA ATCCTGGAAT CTGGGAATGT TAATGATTAT GAAGTTGTGT	180
ATCCACAAAA AGTGCCTGCA TTGCTCAAAG GAGGAGTCA GAATCCTCAG CCAGAGACCA	240
AGTATGAAGA TACAATGCAA TATGAATTTC AAGTGAATGG AGAGCCAGTA GTCCTTCACT	300
TAGAAAGAAA TAAAGGACTT TTTTCAGAAG ATTACACTGA AACTCATTAT GCCCCTGATG	360
GCAGAGAAAT TACAACAAGC CCTCCGGTTC AGGATCACTG CTATTATCAT GGTACATTC	420
AGAATGAAGC TGACTCAAGT GCAATCATCA GTGCATGTGA TGGCTTGAAA GGACATTTC	480

AGCATCAAGG GGAGACATAC TTTATTGAGC CCTTGAAGCT TTTCGACAGT GAATCCCATG	540
CAATCTACAA AGATGAAAAT GTAGAAAACG AGGATGAGAC CCCCAGAAACC TGTGGGGTAA	600
CCGAGACTAC TTGGGAGTCA GATGAGTCCA TCGAAAAGAC CTCTCAGTTA ACTAACACTC	660
CTGAACAAGA CGGGTACTTG CAGGCCAAAA AATACATCGA GTTTTACGTG GTTGTGGACA	720
ACAGAATGTA CAGGTATTAC AAACGCAATG AACCTGCTAT AAAAAGAAGA GTATATGAAA	780
TGGTCAACGC TGTAATACG TACAGACCTT TGAAAATTCA CATAACACTG ATTGGCCTAG	840
AAATTTGGTC CAACGATGAT AAGTTTGAAG TGAAGCCAGT AGCGGGTGCC ACTTTGAAAT	900
CATTTGAGA TTGGAGAGAA ACAGTTTTGC TGCCACGCAA AAGGAATGAT AACGCTCAGT	960
TACTCACGGG CATTGACTTC AATGGAAC TGTTGGGAAT TGCTTACAG GGCACCCTCT	1020
GCACTCAGAA TTCTGTAGCA GTTGTTTCAG ATTATAACCG AAAAATAAGC ATGGTGGCAT	1080
CTACAATGGC CCATGAGTTG GGTCATAATC TGGGCCTTCA TCATGACGGA GCTTCCTGTA	1140
TTTGAGTCT TAGACCATGC ATTATGTCTA AGGGACGGAC TGCACCTGCC TTTCAGTTCA	1200
GCTCTGTAG TGTCCGGGAG TATCGGGAGT ATCTTCTTAG AGAAAGACCA CAATGCATTC	1260
TCAACAAACC CTTGAGCACA GATACTGTTT CACCTGCAAT TTGTGGAAAT TACTTTGTGG	1320
AGGAGGGAGA AGAATGTGAC TGTGGCTCTC CTGCGGATTG TCAAAGTGCC TGCTGCGATG	1380
CTGCAACTTG TAAGTTTAAG GGAGAAGAAG CAGAATGCCG GGCAGCAAAG GATGACTGTG	1440
ACTTGCCTGA ACTCTGCACT GGCCGATCTG TGGAGTGTCC CACGGACAGC TTGCAGAGGA	1500
ATGGACATCC ATGTCAAAAC AACAAAGGTT ACTGCTACAA TGGGGCATGT CCCACCTTCA	1560
CAAACCAATG TATTGCTCTC ATGGGGACAG ATTTTACTGT GAGTCCAGAT GGATGTTTTG	1620
ACTTGAACGT GAGAGGGAAT TGATGTAAGC CACTGCAGAA AGGAAAATGG TGCAAAGATT	1680

CCATGTGCAG CAAAGGATGT AAAGTGTGGC AGATTATACT GCACAGAGAG AGACACAATG	1740
TCATGCCGAT TCCCACTGGA CCCAGATGGT GTTAATGGCT GAACCTGGAA CAAAATGTGG	1800
AGATGGAATG GTGTGCAGCA ACGGTCAGTG TGTTAATGTG CAGACAGCCT ACTGATCAAG	1860
CACTGGCTTC TCTCAATTG ATTTTGGAGA TCCTCCTTCC AGAACGCTTC CCTCAAGTCC	1920
AAAGAGACCC ATCTGTCTTT ATCCTACTAG TAAATCACTC TTAGCTTTCA GATGGTATCT	1980
AAAATTTATA ATATTTCTTC TCCATAATTT AAAGTGGTAA TCTTTTGCTA AAATCAGACC	2040
TTTTCCCTGC CACAAAGCTC CATGGTCATG TACAGCACCA AAGGCTTATT TGCGAATAAG	2100
AAAAAAAAAT GGCAATTTTA CAGTTTCCCA ATTGCAATGC ATATTGAATG CAACAAGCTC	2160
TGCCCTTTGA GCTGGCGTAT TCAAAGGCAA TGTCCTCTCT CCCAAAATTA TACGCTGGCT	2220
TTCCAAGATG TAGCTGCTTC CATCAATAAA CTATTCTCAT TCTGAAAAAA AAAAAAAAAA	2280
AAGTCGAC	2288

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ile	Gln	Ala	Leu	Val	Ile	Ile	Cys	Leu	Val	Val	Phe	Pro	Tyr
1				5				10					15	

Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu
 20 25 30

Val Val Tyr Pro Gln Lys Val Pro Ala Leu Leu Lys Gly Gly Val Gln
 35 40 45

Asn Pro Gln Pro Glu Thr Lys Tyr Glu Asp Thr Met Gln Tyr Glu Phe
 50 55 60

Gln Val Asn Gly Glu Pro Val Val Leu His Leu Glu Arg Asn Lys Gly
 65 70 75 80

Leu Phe Ser Glu Asp Tyr Thr Glu Thr His Tyr Ala Pro Asp Gly Arg
 85 90 95

Glu Ile Thr Thr Ser Pro Pro Val Gln Asp His Cys Tyr Tyr His Gly
 100 105 110

Tyr Ile Gln Asn Glu Ala Asp Ser Ser Ala Ile Ile Ser Ala Cys Asp
 115 120 125

Gly Leu Lys Gly His Phe Lys His Gln Gly Glu Thr Tyr Phe Ile Glu
 130 135 140

Pro Leu Lys Leu Phe Asp Ser Glu Ser His Ala Ile Tyr Lys Asp Glu
 145 150 155 160

Asn Val Glu Asn Glu Asp Glu Thr Pro Glu Thr Cys Gly Val Thr Glu
 165 170 175

Thr Thr Trp Glu Ser Asp Glu Ser Ile Glu Lys Thr Ser Gln Leu Thr
 180 185 190

Asn Thr Pro Glu Gln Asp Gly Tyr Leu Gln Ala Lys Lys Tyr Ile Glu
 195 200 205

Phe Tyr Val Val Val Asp Asn Arg Met Tyr Arg Tyr Tyr Lys Arg Asn
 210 215 220

Glu Pro Ala Ile Lys Arg Arg Val Tyr Glu Met Val Asn Ala Val Asn

225	230	235	240
Thr Tyr Arg Pro Leu Lys Ile His Ile Thr Leu Ile Gly Leu Glu Ile			
245	250	255	
Trp Ser Asn Asp Asp Lys Phe Glu Val Lys Pro Val Ala Gly Ala Thr			
260	265	270	
Leu Lys Ser Phe Arg Asp Trp Arg Glu Thr Val Leu Leu Pro Arg Lys			
275	280	285	
Arg Asn Asp Asn Ala Gln Leu Leu Thr Gly Ile Asp Phe Asn Gly Thr			
290	295	300	
Val Val Gly Ile Ala Tyr Thr Gly Thr Leu Cys Thr Gln Asn Ser Val			
305	310	315	320
Ala Val Val Gln Asp Tyr Asn Arg Lys Ile Ser Met Val Ala Ser Thr			
325	330	335	
Met Ala His Glu Leu Gly His Asn Leu Gly Leu His His Asp Gly Ala			
340	345	350	
Ser Cys Ile Cys Ser Leu Arg Pro Cys Ile Met Ser Lys Gly Arg Thr			
355	360	365	
Ala Pro Ala Phe Gln Phe Ser Ser Cys Ser Val Arg Glu Tyr Arg Glu			
370	375	380	
Tyr Leu Leu Arg Glu Arg Pro Gln Cys Ile Leu Asn Lys Pro Leu Ser			
385	390	395	400
Thr Asp Thr Val Ser Pro Ala Ile Cys Gly Asn Tyr Phe Val Glu Glu			
405	410	415	
Gly Glu Glu Cys Asp Cys Gly Ser Pro Ala Asp Cys Gln Ser Ala Cys			
420	425	430	
Cys Asp Ala Ala Thr Cys Lys Phe Lys Gly Glu Glu Ala Glu Cys Arg			
435	440	445	

Ala Ala Lys Asp Asp Cys Asp Leu Pro Glu Leu Cys Thr Gly Arg Ser
450 455 460

Val Glu Cys Pro Thr Asp Ser Leu Gln Arg Asn Gly His Pro Cys Gln
465 470 475 480

Asn Asn Lys Gly Tyr Cys Tyr Asn Gly Ala Cys Pro Thr Phe Thr Asn
485 490 495

Gln Cys Ile Ala Leu Met Gly Thr Asp Phe Thr Val Ser Pro Asp Gly
500 505 510

Cys Phe Asp Leu Asn Val Arg Gly Asn
515 520

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACGTCA ACAGGAGAAA AGCTCAGGTT GGCTTGGAAG CAGAAAGAGA TTCCTGTCCA	60
CCAGTCCAAT CCAGGCTCCA AAATGATCCA AGCTCTCTTG GTAATTATAT GCTTAGTGGT	120
TTTTCATAT CAAGGGAGCT CTATAATCCT GGAATCTGGG AATGTTAATG ATTATGAAGT	180
TGTGTATCCA CAAAAGTGC CTGCATTGCT CAAAGGAGGA GTTCAGAATC CTCAGCCAGA	240
GACCAAGTAT GAAGATACAA TGCAATATGA ATTTCAAGTG AATGGAGAGC CAGTAGTCCT	300

TCACCTAGAA AGAAATAAAG GACTTTTTTC AGAAGATTAC ACTGAAACTC ATTATGCCCC	360
TGATGGCAGA GAAATTACAA CAAGCCCTCC GGTTCAGGAT CACTGCTATT ATCATGGTTA	420
CATTCAGAAT GAAGCTGACT CAAGTGCAAT CATCAGTGCA TGTGATGGCT TGAAAGGACA	480
TTTCAAGCAT CAAGGGGAGA CATACTTTAT TGAGCCCTTG AAGCTTTTCG ACAGTGAATC	540
CCATGCAATC TACAAAGATG AAAATGTAGA AAACGAGGAT GAGACCCCG AAACCTGTGG	600
GGTAACCGAG ACTACTTGGG AGTCAGATGA GTCCATCGAA AAGACCTCTC AGTTAACTAA	660
CACTCCTGAA CAAGACGGGT ACTTGCAGGC CAAAAAATAC ATCGAGTTT ACGTGGTTGT	720
GGACAACAGA ATGTACAGGT ATTACAAACG CAATGAACCT GCTATAAAAA GAAGAGTATA	780
TGAAATGGTC AACGCTGTAA ATACGAAGTA CAGACCTTTG AAAATTCACA TAACACTGAT	840
TGGCCTAGAA ATTTGGTCCA ACGATGATAA GTTTGAAGTG AAGCCAGTAG CGGGTGCCAC	900
TTTGAAATCA TTTCGAGATT GGAGAGAAAC AGTTTTGCTG CCACGCAAAA GGAATGATAA	960
CGCTCAGTTA CTCACGGGCA TTGACTTCAA TGGAACTGTT GTGGGAATTG CTTACACGGG	1020
CACCCTCTGC ACTCAGAATT CTGTAGCAGT GTTTCAGGAT TATAACCGAA AAATAAGCAT	1080
GGTGGCATCT ACAATGGCCC ATGAGTTGGG TCATAATCTG GGCCTTCATC ATGACGGAGC	1140
TTCTGTATT TGCAGTCTTA GACCATGCAT TATGTCTAAG GGACGGACTG CACCTGCCTT	1200
TCAGTTCAGC TCTTGTAGTG TCCGGGAGTA TCGGGAGTAT CTCTTAGAG AAAGACCACA	1260
ATGCATTCTC AACAAACCCT TGAGCACAGA TACTGTTTCA CCTGCAATTT GTGGAAATTA	1320
CTTTGTGGAG GAGGGAGAAG AATGTGACTG TGGCTCTCCT GCGGATTGTC AAAGTGCCTG	1380
CTGCGATGCT GCAACTTGTA AGTTTAAGGG AGAAGAAGCA GAATGCCGGG CAGCAAAGGA	1440
TGACTGTGAC TTGCCTGAAC TCTGCACTGG CCGATCTGTG GAGTGTCCCA CGGACAGCTT	1500

GCAGAGGAAT GGACATCCAT GTCAAAACAA CAAAGGTTAC TGCTACAATG GGGCATGTCC 1560

CACCTTCACA AACCAATGTA TTGCTCTCAT GGGGACAGAT TTTACTGTGA GTCCAGATGG 1620

ATGTTTTGAC TTGAACGTGA GAGGGAATGA TGTAAGCCAC TGCAGAAAGG AAAATGGTGC 1680

AAAGATTCCA TGTGCAGCAA AGGATGTAAA GTGTGGCAGG TTATACTGCA CAGAGAGAGA 1740

CACAATGTCA TGCCGATTCC CACTGGACCC AGATGGTGTA ATGGCTGAAC CTGGAACAAA 1800

ATGTGGAGAT GGAATGGTGT GCAGCAACGG TCAGTGTGTT AATGTGCAGA CAGCCTACTG 1860

ATCAAGCACT GGCTTCTCTC AATTTGATTT TGGAGATCCT CCTTCCAGAA CGCTTCCCTC 1920

AAGTCCAAAG AGACCCATCT GTCTTTATCC TACTAGTAAA TCACTCTTAG CTTTCAGATG 1980

GTATCTAAAA TTTATAATAT TTCTTCTCCA TAATTTAAAC TGGTAATCTT TTGCTAAAAAT 2040

CAGACCTTTT CCCTGCCACA AAGCTCCATG GTCATGTACA GCACCAAAGG CTTATTTGCG 2100

AATAAGAAAA AAAAATGGCA ATTTTACAGT TTCCAATTG CAATGCATAT TGAATGCAAC 2160

AAGCTCTGCC CTTTGAGCTG GCGTATTCAA AGGCAATGCT CCCTCTCCCA AAATTATACG 2220

CTGGCTTTCC AAGATGTAGC TGCTTCCATC AATAAACTAT TCTCATTCTG AAAAAAAAAA 2280

AAAAAAAAAA AAAAAAAAAA AAAGTCGAC 2309

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ile Gln Ala Leu Leu Val Ile Ile Cys Leu Val Val Phe Pro Tyr
1 5 10 15

Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu
20 25 30

Val Val Tyr Pro Gln Lys Val Pro Ala Leu Leu Lys Gly Gly Val Gln
35 40 45

Asn Pro Gln Pro Glu Thr Lys Tyr Glu Asp Thr Met Gln Tyr Glu Phe
50 55 60

Gln Val Asn Gly Glu Pro Val Val Leu His Leu Glu Arg Asn Lys Gly
65 70 75 80

Leu Phe Ser Glu Asp Tyr Thr Glu Thr His Tyr Ala Pro Asp Gly Arg
85 90 95

Glu Ile Thr Thr Ser Pro Pro Val Gln Asp His Cys Tyr Tyr His Gly
100 105 110

Tyr Ile Gln Asn Glu Ala Asp Ser Ser Ala Ile Ile Ser Ala Cys Asp
115 120 125

Gly Leu Lys Gly His Phe Lys His Gln Gly Glu Thr Tyr Phe Ile Glu
130 135 140

Pro Leu Lys Leu Phe Asp Ser Glu Ser His Ala Ile Tyr Lys Asp Glu
145 150 155 160

Asn Val Glu Asn Glu Asp Glu Thr Pro Glu Thr Cys Gly Val Thr Glu
165 170 175

Thr Thr Trp Glu Ser Asp Glu Ser Ile Glu Lys Thr Ser Gln Leu Thr
180 185 190

Asn Thr Pro Glu Gln Asp Gly Tyr Leu Gln Ala Lys Lys Tyr Ile Glu
195 200 205

Phe Tyr Val Val Val Asp Asn Arg Met Tyr Arg Tyr Tyr Lys Arg Asn
 210 215 220
 Glu Pro Ala Ile Lys Arg Arg Val Tyr Glu Met Val Asn Ala Val Asn
 225 230 235 240
 Thr Lys Tyr Arg Pro Leu Lys Ile His Ile Thr Leu Ile Gly Leu Glu
 245 250 255
 Ile Trp Ser Asn Asp Asp Lys Phe Glu Val Lys Pro Val Ala Gly Ala
 260 265 270
 Thr Leu Lys Ser Phe Arg Asp Trp Arg Glu Thr Val Leu Leu Pro Arg
 275 280 285
 Lys Arg Asn Asp Asn Ala Gln Leu Leu Thr Gly Ile Asp Phe Asn Gly
 290 295 300
 Thr Val Val Gly Ile Ala Tyr Thr Gly Thr Leu Cys Thr Gln Asn Ser
 305 310 315 320
 Val Ala Val Val Gln Asp Tyr Asn Arg Lys Ile Ser Met Val Ala Ser
 325 330 335
 Thr Met Ala His Glu Leu Gly His Asn Leu Gly Leu His His Asp Gly
 340 345 350
 Ala Ser Cys Ile Cys Ser Leu Arg Pro Cys Ile Met Ser Lys Gly Arg
 355 360 365
 Thr Ala Pro Ala Phe Gln Phe Ser Ser Cys Ser Val Arg Glu Tyr Arg
 370 375 380
 Glu Tyr Leu Leu Arg Glu Arg Pro Gln Cys Ile Leu Asn Lys Pro Leu
 385 390 395 400
 Ser Thr Asp Thr Val Ser Pro Ala Ile Cys Gly Asn Tyr Phe Val Glu
 405 410 415
 Glu Gly Glu Glu Cys Asp Cys Gly Ser Pro Ala Asp Cys Gln Ser Ala

430

445

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1820 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTGACGACA TTTCAAGCAT CAAGGGGAGA CATACTTTAT TGAGCCCTTG AAGCTTTTCG	60
ACAGTGAATC CCATGCAATC TACAAAGATG AAAATGTAGA AAACGAGGAT GAGACCCCCG	120
AAACCTGTGG GGTAACCGAG ACTACTTGGG AGTCAGATGA GTCCATTGAA AAGACCTCTC	180
AGTTAACTAA CACTCCTGAA CAAGACGGGT ACTTGCAGGC CAAAAATAC ATCGAGTTTT	240
ACGTGGTTGT GGACAACAGA ATGTACAGGT ATTACAAACG CAATGAACCT GCTATAAAAA	300
GAAGAGTATA TGAAATGGTC AACGCTGTAA ATACGAAGTA CAGACCTTG AAAATTCACA	360
TAACTACTGAT TGGCCTAGAA ATTTGGTCCA ACGATGATAA GTTTGAAGTG AAGCCAGTAG	420
CGGGTGCCAC TTGAAATCA TTTCGAGATT GGAGAGAAAC AGTTTGTCTG CCACGCAAAA	480
GGAATGATAA CGCTCAGTTA CTCACGGGCA TTGACTTCAA TGGAACTGTT GTGGGAATTG	540
CTTACACGGG CACCCTCTGC ACTCAGAATT CTGTAGCAGT TGTTCAGGAT TATAACCGAA	600
AAATAAGCAT GGTGGCATCT ACAATGGCCC ATGAGTTGGG TCATAATCTG GGCATTTCATC	660
ATGACGGAGC TTCCTGTATT TGCAGTCTTA AACCATGCAT TATGTCTAAG GGACGGACTG	720
CACCTGCCTT TCAGTTCAGC TCTTGTAGTG TCCGGGAGTA TCGGGAGTAT CTTCTTAGAA	780
AAAGACCACA ATGCATTCTC AACAAACCTT TGAGCACAGA TATTGTTTCA CCTGCAATTT	840
GTGGAAATTA CTTTGTGGAG GAGGGAGAAG AATGTGACTG TGGCTCTCCT GCGGATTGTC	900
AAAGTGCTG CTGCAATGCT GCAACTTGTA AGTTTAAGGG AGAAGAAGCA GAATGCCGGG	960
CAGCAAAGGA TGA CTGTGAC TTGCCTGAAC TCTGCACTGG CCGATCTGTG GAGTGTCCTA	1020

CGGACAGCTT GCAGAGGAAT GGACATCCAT GTCAAAACAA CAAAGGTTAC TGCTACAATG 1080

GGGCATGTCC CACCTTCACA AACCAATGTA TTGCTCTCAT GGGGACAGAT TTTACTGTGA 1140

GTCCAGATGG ATGTTTTGAC TTGAACGTGA GAGGGAATGA TGTAAGCCAC TGCAGAAAGG 1200

AAAATGGTGC AAAGATTCCA TGTGCAGCAA AGGATGTAAA GTGTGGCAGG TTATACTGCA 1260

CAGAGAGAAA CACAATGTCA TGCCGATTCC CACTGGACCC AGATGGTGTA ATGGCTGAAC 1320

CTGGAACAAA ATGTGGAGAT GGAATGGTGT GCAGCAACGG TCAGTGTGTT AATGTGCAGA 1380

CAGCCTACTG ATCAAGCACT GGCTTCTCTC AATTGATTT TGGAGATCCT CCTCCAGAA 1440

CGCTTCCCTC AAGTCCAAAG AGACCCATCT GTCTTTATCC TACTAGTAAA TCACTCTTAG 1500

CTTTCAGATG GTATCTAAAA TTTATAATAT TTCTTCTCCA TAATTTAAAC TGTAATCTT 1560

TTGCTAAAAT CAGACCTTTT CCTGCCACA AAGCTCCATG GTCATGTACA GTACCAAAGG 1620

CTTATTTGCT AACACGAAAA AAAATGGCCA TTTTACCGTT TGCCAATTGC AATTCACATT 1680

TAATGCAACA AGCTCTGCCC TTTGAGCTGG CGTATTCAA GGCAATGCTC CCTCTCCCAA 1740

AATTATATGC TGGCTTTCCA AGATGTAGCT GCTTCCATCA ATAACTATT CTCATTCTGA 1800

AAAAAAAAAA AAAAGTCGAC 1820

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Arg His Phe Lys His Gln Gly Glu Thr Tyr Phe Ile Glu Pro Leu
1 5 10 15

Lys Leu Phe Asp Ser Glu Ser His Ala Ile Tyr Lys Asp Glu Asn Val
20 25 30

Glu Asn Glu Asp Glu Thr Pro Glu Thr Cys Gly Val Thr Glu Thr Thr
35 40 45

Trp Glu Ser Asp Glu Ser Ile Glu Lys Thr Ser Gln Leu Thr Asn Thr
50 55 60

Pro Glu Gln Asp Gly Tyr Leu Gln Ala Lys Lys Tyr Ile Glu Phe Tyr
65 70 75 80

Val Val Val Asp Asn Arg Met Tyr Arg Tyr Tyr Lys Arg Asn Glu Pro
85 90 95

Ala Ile Lys Arg Arg Val Tyr Glu Met Val Asn Ala Val Asn Thr Lys
100 105 110

Tyr Arg Pro Leu Lys Ile His Ile Thr Leu Ile Gly Leu Glu Ile Trp
115 120 125

Ser Asn Asp Asp Lys Phe Glu Val Lys Pro Val Ala Gly Ala Thr Leu
130 135 140

Lys Ser Phe Arg Asp Trp Arg Glu Thr Val Leu Leu Pro Arg Lys Arg
145 150 155 160

Asn Asp Asn Ala Gln Leu Leu Thr Gly Ile Asp Phe Asn Gly Thr Val
165 170 175

Val Gly Ile Ala Tyr Thr Gly Thr Leu Cys Thr Gln Asn Ser Val Ala
180 185 190

Val Val Gln Asp Tyr Asn Arg Lys Ile Ser Met Val Ala Ser Thr Met
195 200 205

Ala His Glu Leu Gly His Asn Leu Gly Ile His His Asp Gly Ala Ser
 210 215 220

Cys Ile Cys Ser Leu Lys Pro Cys Ile Met Ser Lys Gly Arg Thr Ala
 225 230 235 240

Pro Ala Phe Gln Phe Ser Ser Cys Ser Val Arg Glu Tyr Arg Glu Tyr
 245 250 255

Leu Leu Arg Lys Arg Pro Gln Cys Ile Leu Asn Lys Pro Leu Ser Thr
 260 265 270

Asp Ile Val Ser Pro Ala Ile Cys Gly Asn Tyr Phe Val Glu Glu Gly
 275 280 285

Glu Glu Cys Asp Cys Gly Ser Pro Ala Asp Cys Gln Ser Ala Cys Cys
 290 295 300

Asn Ala Ala Thr Cys Lys Phe Lys Gly Glu Glu Ala Glu Cys Arg Ala
 305 310 315 320

Ala Lys Asp Asp Cys Asp Leu Pro Glu Leu Cys Thr Gly Arg Ser Val
 325 330 335

Glu Cys Pro Thr Asp Ser Leu Gln Arg Asn Gly His Pro Cys Gln Asn
 340 345 350

Asn Lys Gly Tyr Cys Tyr Asn Gly Ala Cys Pro Thr Phe Thr Asn Gln
 355 360 365

Cys Ile Ala Leu Met Gly Thr Asp Phe Thr Val Ser Pro Asp Gly Cys
 370 375 380

Phe Asp Leu Asn Val Arg Gly Asn Asp Val Ser His Cys Arg Lys Glu
 385 390 395 400

Asn Gly Ala Lys Ile Pro Cys Ala Ala Lys Asp Val Lys Cys Gly Arg
 405 410 415

Leu Tyr Cys Thr Glu Arg Asn Thr Met Ser Cys Arg Phe Pro Leu Asp

420

425

430

Pro Asp Gly Val Met Ala Glu Pro Gly Thr Lys Cys Gly Asp Gly Met

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Val Cys Ser Asn Gly Gln Cys Val Asn Val Gln Thr Ala Tyr

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2359 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCGACCTCA GGTGGCTTG GAAGCAGAAA GAGATTCCTA TCCACCACTC CAATCCAGGC	60
TCCAAAATGA TCCAAGCTCT CTTGGTAGCT ATATGCTTAG CGGTTTTTCC ATATCAAGGG	120
AGCTCTATAA TCCTGGAATC CGGGAATGTT AATGATTATG AAGTAGTGTA TCCACAAAAA	180
GTGCCTGCAT TGTCCAAAGG AGGAGTTCAG AATCCTCAGC CAGAGACCAA GTATGAAGAT	240
ACAATGCAAT ATGAATTTCA AGTGAATGGA GAGCCAGTAG TCCTTCACCT AGAAAGAAAT	300
AAAGGACTTT TTTCAGAAGA TTACTGAA ACTCATTATG CCTCTGATGG CAGAGAAATT	360
ACAACAAGCC CACTCGTTCA GGATCACTGC TATTATCATG GTTACATTCA GAATGAAGCT	420
GACTCAAGTG CAGTCATCAG TGCATGCGAT GGCTTGAAAG GACATTTCCA GCTTCAAGGG	480
GAGACATACT TTATTGAACC CTTGAAGATT TCCGACAGTG AAGCCCATGC AATCTACAAA	540
GATGAAAATG TAGAAAACGA GGATGAGACC CCCGAAACCT GTGGGGTAAC CGAGACTACT	600
TGGGAGTCAG ATGAGTCCAT TGAAAAGACC TCTCAGTTAG ACGACGACGA CAAGCGGCCG	660

CCAAC TAACA CTCCTGAACA AGACAGGTAC TTGCAGGCCA AAAAATACCT CGAGTTTAC	720
GTGGTTGTGG ACAACATAAT GTACAGGCAT TACAAACGCG ATAAACCTGT TATAAAAAGA	780
AGAGTATATG AAATGATCAA CACTATGAAT ATGGTGTACA ATCGTTTGAA TTTTCACATA	840
GCACTGATTG GCCTAGAAAT TTGGTCCAAC AGAAATGAGA TTAATGTGCA ATCAGACGTG	900
CAGGCCACTT TGGACTTATT TGGAGAATGG AGAGAAAAAA AATTGCTGCC ACGCAAAAGG	960
AATGATAATG CTCAGTTACT CACGGGTATT GACTTCAAAG GAACTCCTGT AGGACTTGCT	1020
TACATAGGTT CCATCTGCAA TCCGAAGAGT TCTGTAGCAG TTGTTTCAGGA TTATAGCAGT	1080
AGAACAAGCA TGGTGGCAAT TACAATGGCC CATGAGATGG GTCATAATAT GGGCATTCAT	1140
CATGACGGAC CTTCTGTAC TTGTGGTCTT AACAAATGCG TTATGTCTAC AAGACGTACT	1200
GAACCTGCCT ATCAGTTCAG CTCTGTAGT GTCCGGGAAC ATCAGGAGTA TCTTCTTAGA	1260
GACAGACCAC AATGCATTCT CAACAAACCC TTGAGCACAG ATATTGTTTC ACCTCCAATT	1320
TGTGGAAATA ACTTTGTGGA GGTGGGAGAA GAATGTGACT GTGGCTCTCC TCGCGATTGT	1380
CAAAGTGCCT GCTGCGACGC TACAACTTGT AAATACAAC CTCATGCACA GTGTGACTCC	1440
GAAGGGTGTG GTGAGAAATG CAAATTTAAG GGAGCAGGAG CAGAATGCCG GGCAGCAAAG	1500
GATGACTGTG ACTTGCTGA ACTCTGCACT GGCCAATCTG CTGAGTGTC CACAGACATC	1560
TTCCAGAGGA ATGGACTTCC ATGCCAAAAC AACGAAGGTT ACTGCTACAA TGGGAAATGC	1620
CCCATCATGA CAAACCAATG TATTGCTCTC CGGGGACCAG GTGTAAAAGT ATCTCGAGAT	1680
AGCTGTTTTA CATTGAACCA GAGAACCACT GGTGTGGCT TGTGCAGAAT GGAATATGGT	1740
AGAAAGATTC CATGTGCAGC AAAGGATGTA AAGTGTGGCA GGTATTTTTG CAAAAAGGA	1800
AACTCGATGA TATGCAACTG CTCAGTTTCA CCACGTGACC CAAGTTATGG AATGGTTGAA	1860
CCTGGAACAA AATGTGGAGA TGAATGGTG TGCAGCAACA GGCAGTGTGT TGATGTGAAG	1920
ACAGCCTACT GATCAAGCAC TGGCTTCTCT CAATTTGATT TTGGAGGTCC TCCTTCCAGA	1980
ACGCTTCCCT CAAGTCCAAA GAGACCCATC TGTCTTTATC CTA TAGTAA ATCACTCTTA	2040

GCTTTCAGAT GGTATCTAAA ATTTAAAATA TTTCTTCTCC ATAATTTAAA CTGGTAATCT 2100
TTTGCTAAAA TCAGACCTTT TCCCTGCCAC AAAGCTCCAT GGTCAATGTAC AGCACCAAAG 2160
GCTTATTTGC TAACAAGAAA AAAAATGGCC ATTTTACTGT TTGCCAATTG CAATTCACAT 2220
TTAATGCAAC AAGCTCTGCC CTTTGAGCTG GCGTACTCAA AGGCAATGCT CCCTCTCCCA 2280
AAATTATACG CTGGCTTTCC AAGATGTAGC TGCTTCCATC AATAAACTAT TCTCATTCTG 2340
AAAAAAAAAA AAAGTCGAC 2359

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Ile	Gln	Ala	Leu	Leu	Val	Ala	Ile	Cys	Leu	Ala	Val	Phe	Pro	Tyr
1				5					10					15	
Gln	Gly	Ser	Ser	Ile	Ile	Leu	Glu	Ser	Gly	Asn	Val	Asn	Asp	Tyr	Glu
				20				25					30		
Val	Val	Tyr	Pro	Gln	Lys	Val	Pro	Ala	Leu	Ser	Lys	Gly	Gly	Val	Gln
				35				40					45		
Asn	Pro	Gln	Pro	Glu	Thr	Lys	Tyr	Glu	Asp	Thr	Met	Gln	Tyr	Glu	Phe
				50				55					60		
Gln	Val	Asn	Gly	Glu	Pro	Val	Val	Leu	His	Leu	Glu	Arg	Asn	Lys	Gly
65					70					75				80	
Leu	Phe	Ser	Glu	Asp	Tyr	Thr	Glu	Thr	His	Tyr	Ala	Ser	Asp	Gly	Arg
					85					90				95	
Glu	Ile	Thr	Thr	Ser	Pro	Leu	Val	Gln	Asp	His	Cys	Tyr	Tyr	His	Gly

Tyr Ile Gln Asn Glu Ala Asp Ser Ser Ala Val Ile Ser Ala Cys Asp
 115 120 125
 Gly Leu Lys Gly His Phe Glu Leu Gln Gly Glu Thr Tyr Phe Ile Glu
 130 135 140
 Pro Leu Lys Ile Ser Asp Ser Glu Ala His Ala Ile Tyr Lys Asp Glu
 145 150 155 160
 Asn Val Glu Asn Glu Asp Glu Thr Pro Glu Thr Cys Gly Val Thr Glu
 165 170 175
 Thr Thr Trp Glu Ser Asp Glu Ser Ile Glu Lys Thr Ser Gln Leu Asp
 180 185 190
 Asp Asp Asp Lys Arg Pro Pro Thr Asn Thr Pro Glu Gln Asp Arg Tyr
 195 200 205
 Leu Gln Ala Lys Lys Tyr Leu Glu Phe Tyr Val Val Val Asp Asn Ile
 210 215 220
 Met Tyr Arg His Tyr Lys Arg Asp Lys Pro Val Ile Lys Arg Arg Val
 225 230 235 240
 Tyr Glu Met Ile Asn Thr Met Asn Met Val Tyr Asn Arg Leu Asn Phe
 245 250 255
 His Ile Ala Leu Ile Gly Leu Glu Ile Trp Ser Asn Arg Asn Glu Ile
 260 265 270
 Asn Val Gln Ser Asp Val Gln Ala Thr Leu Asp Leu Phe Gly Glu Trp
 275 280 285
 Arg Glu Lys Lys Leu Leu Pro Arg Lys Arg Asn Asp Asn Ala Gln Leu
 290 295 300
 Leu Thr Gly Ile Asp Phe Lys Gly Thr Pro Val Gly Leu Ala Tyr Ile
 305 310 315 320
 Gly Ser Ile Cys Asn Pro Lys Ser Ser Val Ala Val Val Gln Asp Tyr
 325 330 335
 Ser Ser Arg Thr Ser Met Val Ala Ile Thr Met Ala His Glu Met Gly
 340 345 350

His Asn Met Gly Ile His His Asp Gly Pro Ser Cys Thr Cys Gly Ser
355 360 365

Asn Lys Cys Val Met Ser Thr Arg Arg Thr Glu Pro Ala Tyr Gln Phe
370 375 380

Ser Ser Cys Ser Val Arg Glu His Gln Glu Tyr Leu Leu Arg Asp Arg
385 390 395 400

Pro Gln Cys Ile Leu Asn Lys Pro Leu Ser Thr Asp Ile Val Ser Pro
405 410 415

Pro Ile Cys Gly Asn Asn Phe Val Glu Val Gly Glu Glu Cys Asp Cys
420 425 430

Gly Ser Pro Ala Asp Cys Gln Ser Ala Cys Cys Asp Ala Thr Thr Cys
435 440 445

Lys Leu Gln Pro His Ala Gln Cys Asp Ser Glu Gly Cys Cys Glu Lys
450 455 460

Cys Lys Phe Lys Gly Ala Gly Ala Glu Cys Arg Ala Ala Lys Asp Asp
465 470 475 480

Cys Asp Leu Pro Glu Leu Cys Thr Gly Gln Ser Ala Glu Cys Pro Thr
485 490 495

Asp Ile Phe Gln Arg Asn Gly Leu Pro Cys Gln Asn Asn Glu Gly Tyr
500 505 510

Cys Tyr Asn Gly Lys Cys Pro Ile Met Thr Asn Gln Cys Ile Ala Leu
515 520 525

Arg Gly Pro Gly Val Lys Val Ser Arg Asp Ser Cys Phe Thr Leu Asn
530 535 540

Gln Arg Thr Ser Gly Cys Gly Leu Cys Arg Met Glu Tyr Gly Arg Lys
545 550 555 560

Ile Pro Cys Ala Ala Lys Asp Val Lys Cys Gly Arg Leu Phe Cys Lys
565 570 575

Lys Gly Asn Ser Met Ile Cys Asn Cys Ser Val Ser Pro Arg Asp Pro
580 585 590

Ser Tyr Gly Met Val Glu Pro Gly Thr Lys Cys Gly Asp Gly Met Val

595

600

605

Cys Ser Asn Arg Gln Cys Val Asp Val Lys Thr Ala Tyr
610 615 620

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACNCCNGARC ARGAY

15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

RTAYTTYCKR TACAT

15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGACAGGT ACTTGCAGGC CAAA

24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCGAGTTTT ACGTGGTTGT GGAC

24